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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

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101	an statistical analyses, commit that the following items are present in the figure regend, table regend, main text, or Methods section.
n/a	Confirmed
	\square The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
	A description of all covariates tested
	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
So	ftware and code
Poli	cy information about <u>availability of computer code</u>

Data collection

The data from the UK Biobank that support the findings of this study are available upon application (https://www.ukbiobank.ac.uk/register-

Data analysis

We performed all analyses using R version 3.6.1. We made our code accessible at (https://github.com/stejat98/UKB_COVID_XWAS).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

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Please select the o	ne below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.		
∑ Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences		
For a reference copy of	he document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf		
Life scier	nces study design		
All studies must dis	close on these points even when the disclosure is negative.		
Sample size	We analyzed two non-overlapping subsets of the UK Biobank [UKB] cohort (total n=502,655 participants) for which we had data pertaining to COVID-19 testing for tests administered until July 17, 2020 and tests administered between July 18, 2020 and February 2, 2021. We excluded participants whose ethnicity was not known, yielding samples of 9,268 and 38,837 participants, respectively.		
Data exclusions	ta exclusions We excluded participants whose ethnicity was not known.		
Replication We performed a massive sensitivity analysis (vibration of effects [VoE]) to systematically test how associations vary due to combinations of potential confounders. We were not able to use other cohorts to replicate as (to our knowledge) there is no comparable cohort (in size) that COVID-19 outcome and environmental data.			
Randomization	This is not relevant to our study. We performed analyses on observational data from a prospective UK cohort.		
Blinding	This is not relevant to our study. We performed analyses on observational data from a prospective UK cohort.		
We require informati system or method list Materials & ex n/a Involved in th	cell lines cell lines mathematicipants ChIP-seq Flow cytometry MRI-based neuroimaging dother organisms earch participants		
Policy information	about <u>studies involving human research participants</u>		
Population chara	The UK Biobank is a very large and detailed prospective cohort with over 500,000 participants aged 40–69 years (with a roughly even number of men and women).		
Recruitment	Participants living "within a 25-mile radius of any of the 22 assessment centres across the UK were identified from NHS patient registers" (Source: UK Biobank, IJE). In total, around 9 million individuals were invited to participate of which 500,000 participants were recruited. (Source: UK Biobank, IJE). Of these individuals, our analyses focuses on the subset for which COVID-19 test data was available (for around 40,000 individuals from the start of the pandemic till February 2, 2021).		
Ethics oversight	UK Biobank and Harvard University IRB (IRB16-2145)		

Note that full information on the approval of the study protocol must also be provided in the manuscript.